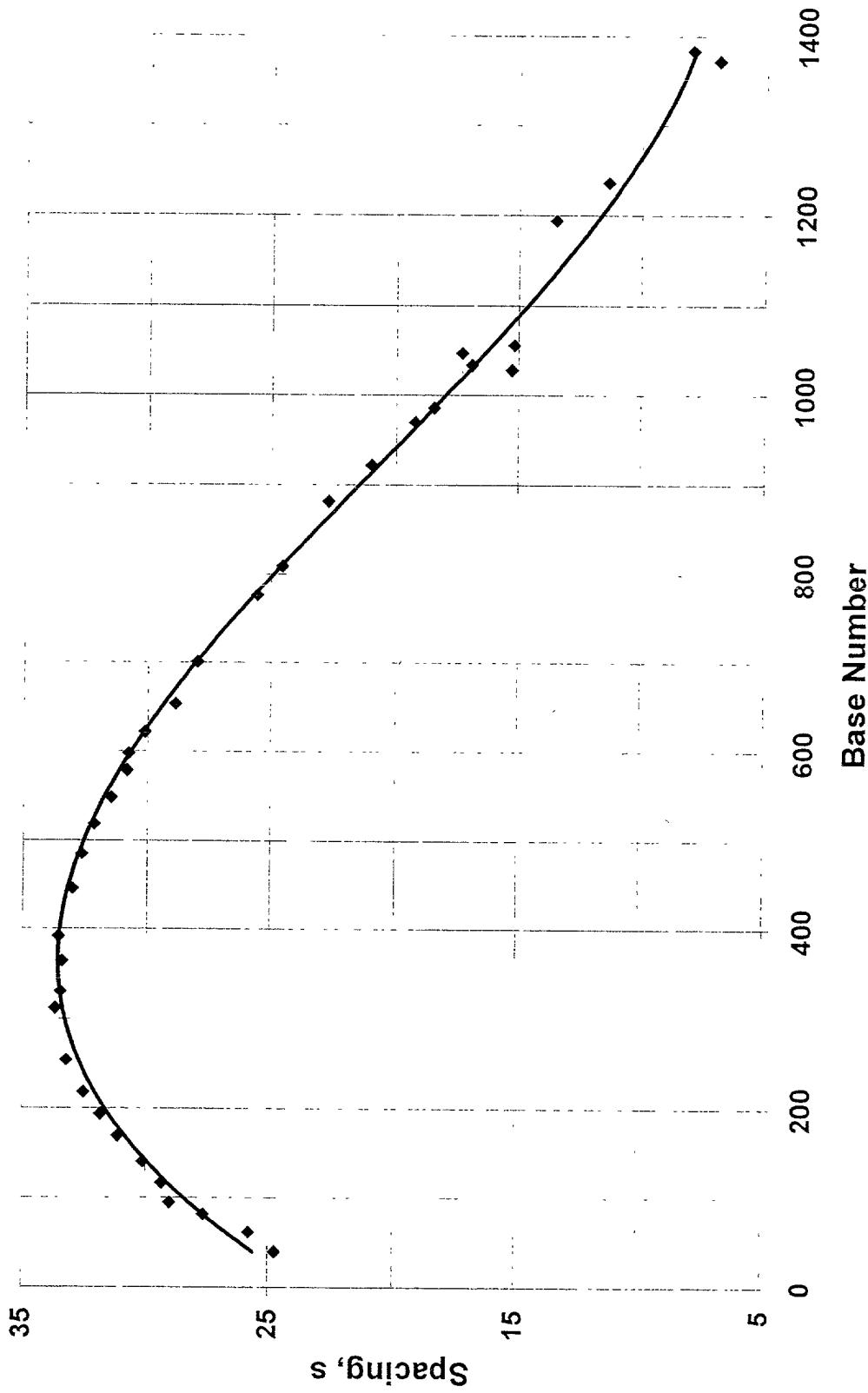


Fig. 1

Spacing Between Adjacent Peaks in the Raw Data  
(M13, T<sub>s</sub> T=6%, 60C, Long Gel)



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Spacing Between Adjacent Bases  
(for Different Number of Peaks Used for Alignment of Raw Data)  
(M13, Long Gel, 55C, T=6%)

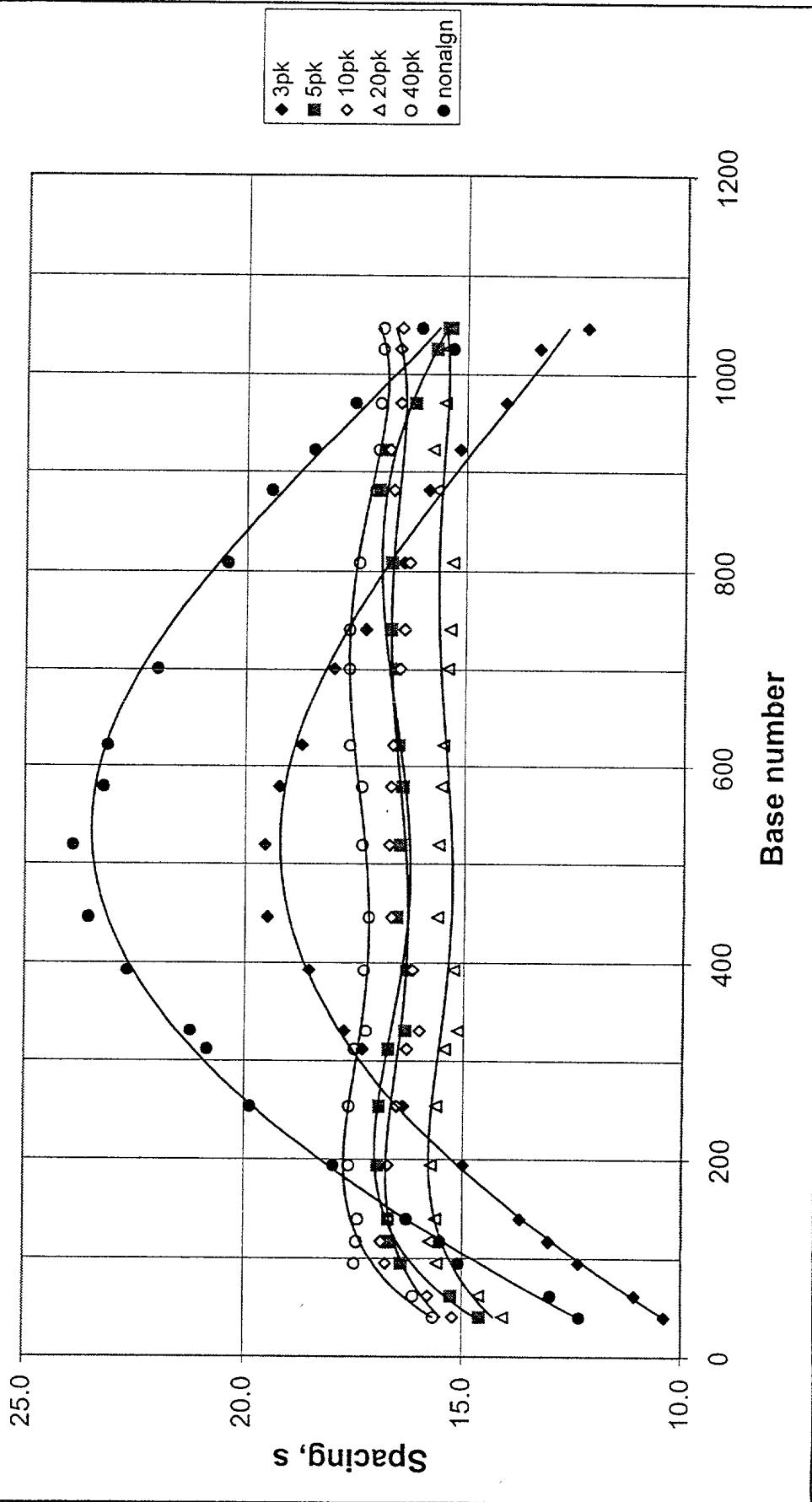
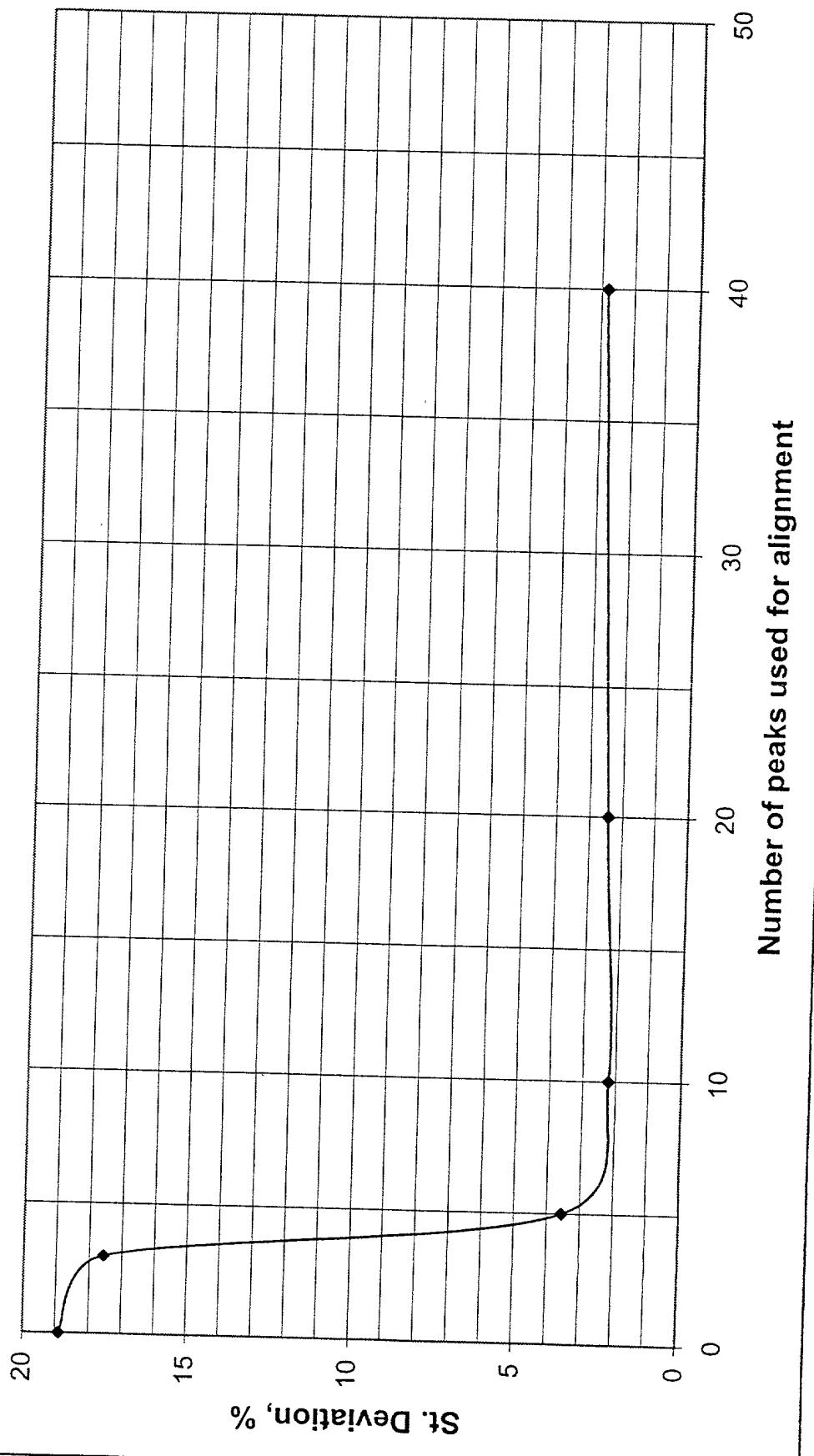


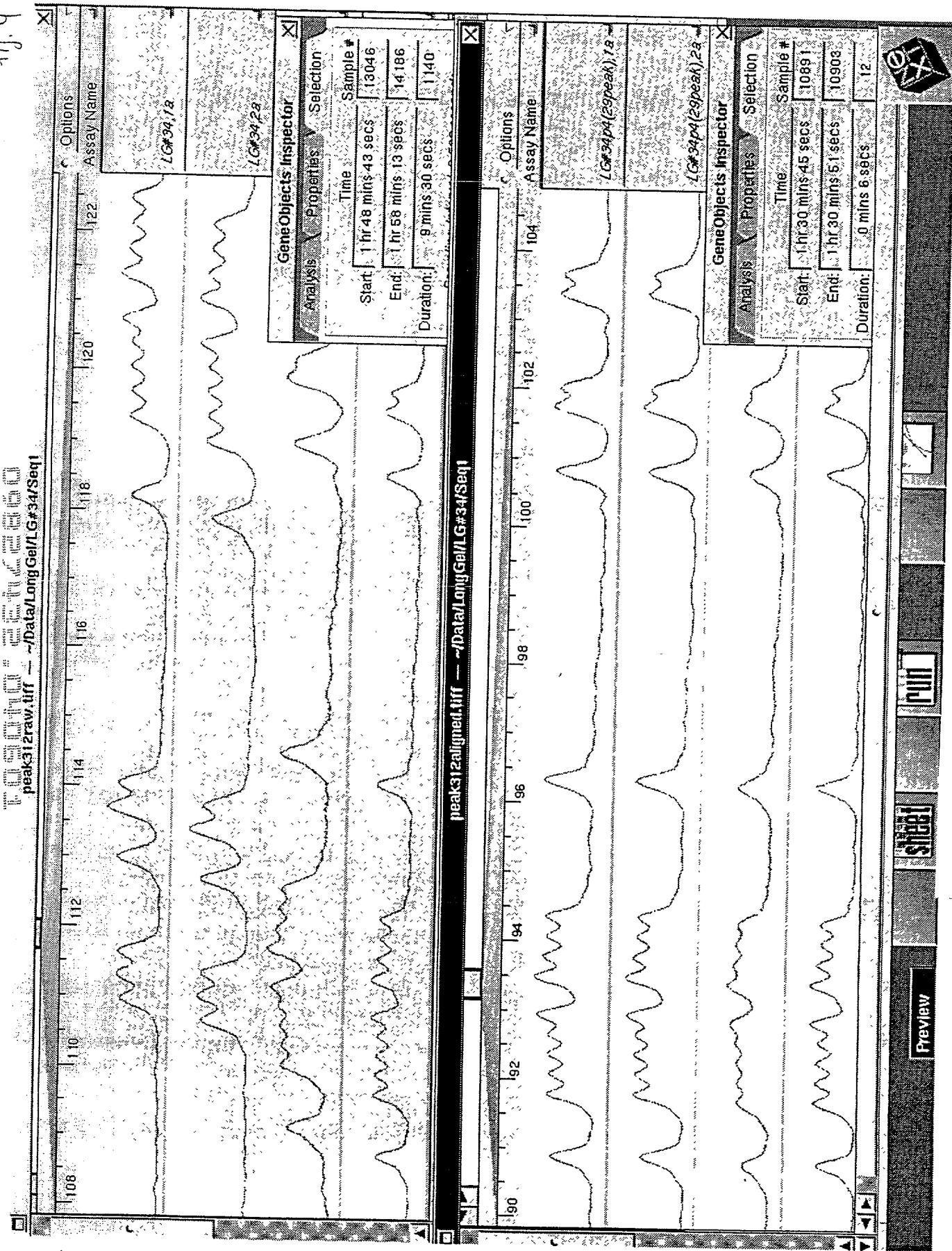
Fig. 3

Standard Deviation (%) of the Spacing Between Adjacent Bases from Average as a Function of Number of Peaks Used as a Reference for Alignment of Raw Data



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Run Time of the BP#1056 in Different Lanes  
(after alignment based on 10 peaks)

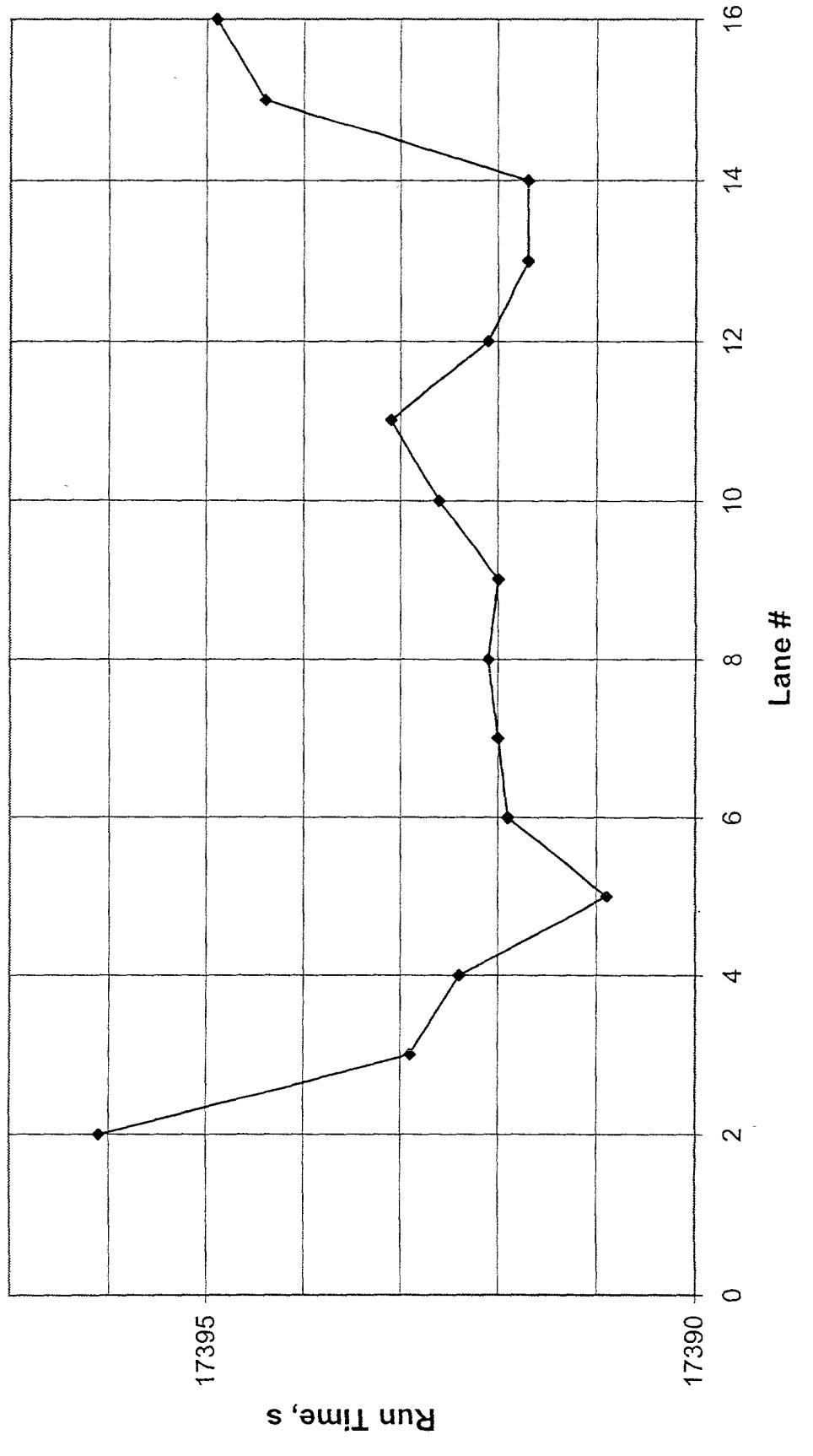
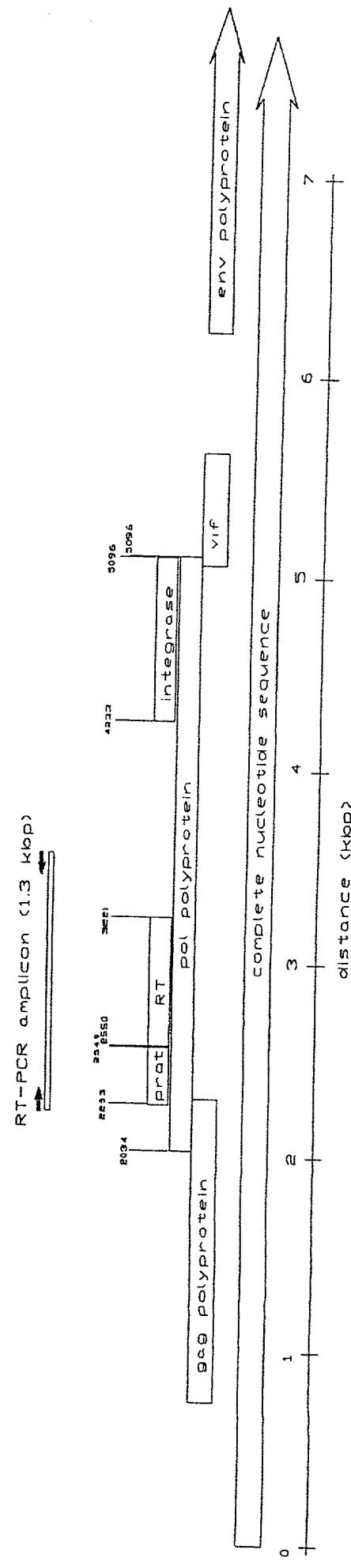
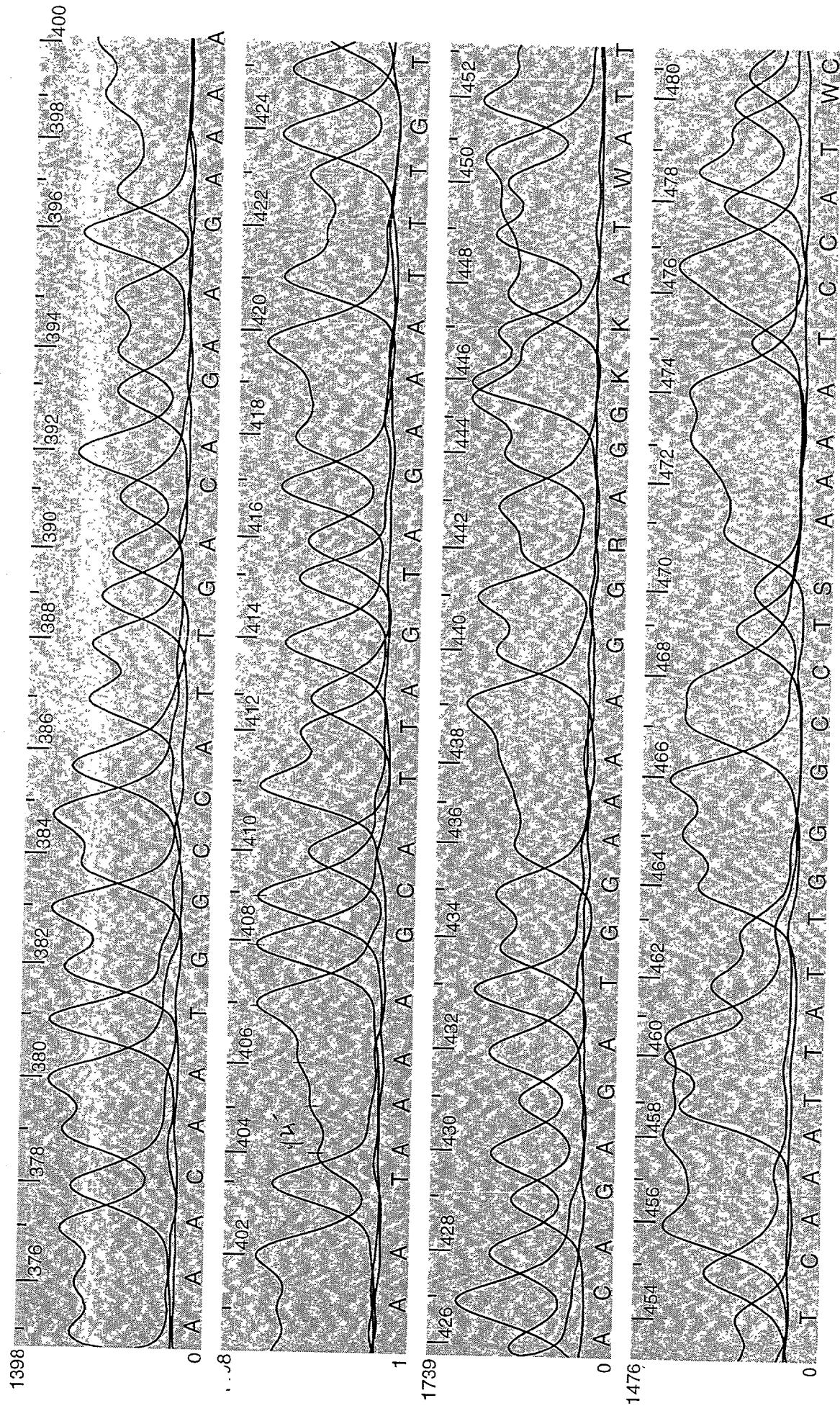
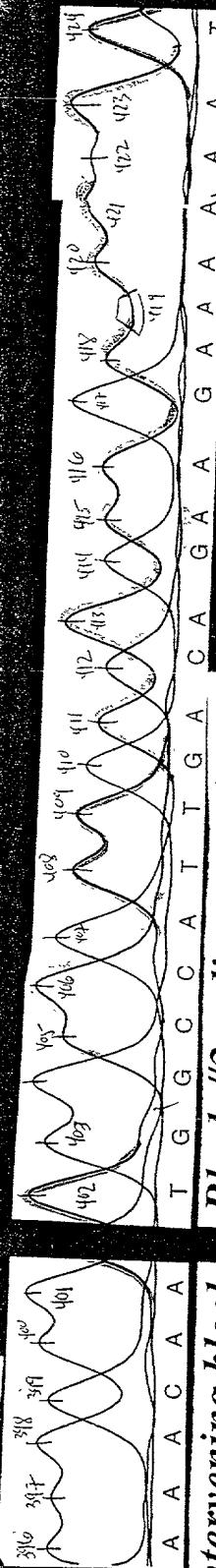


Figure 6



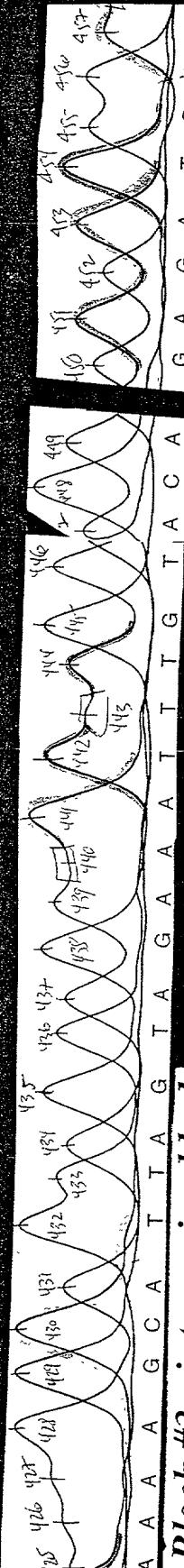
Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc





## Block #1 -

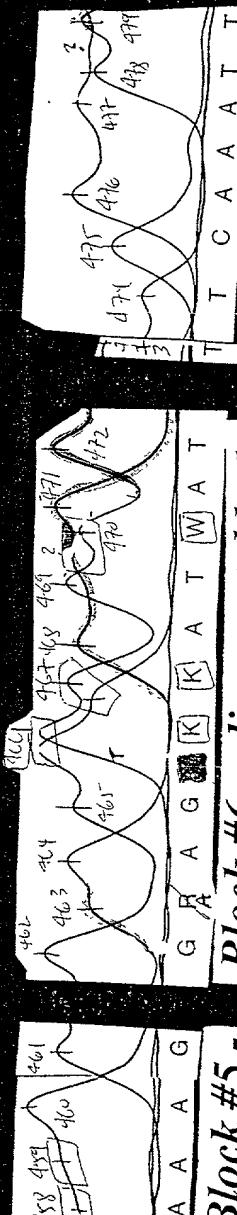
*intervening block*      *Block #2 - alignment block*



### Block #3 - intervening block

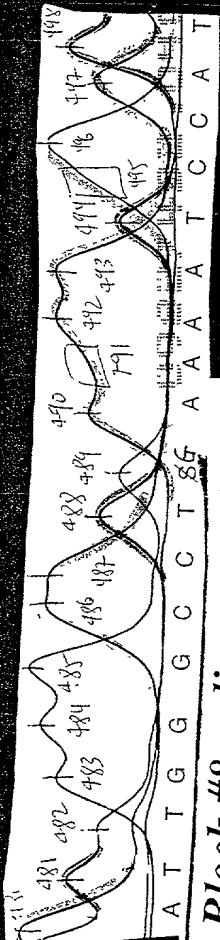
## Block #5 - intervening

## Block #6 - alignment block



## *Block #4 - alignment*

## Block #7 - intervening block



## Block #8 - alignment block

## Block #9 - *introduction block*



### Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

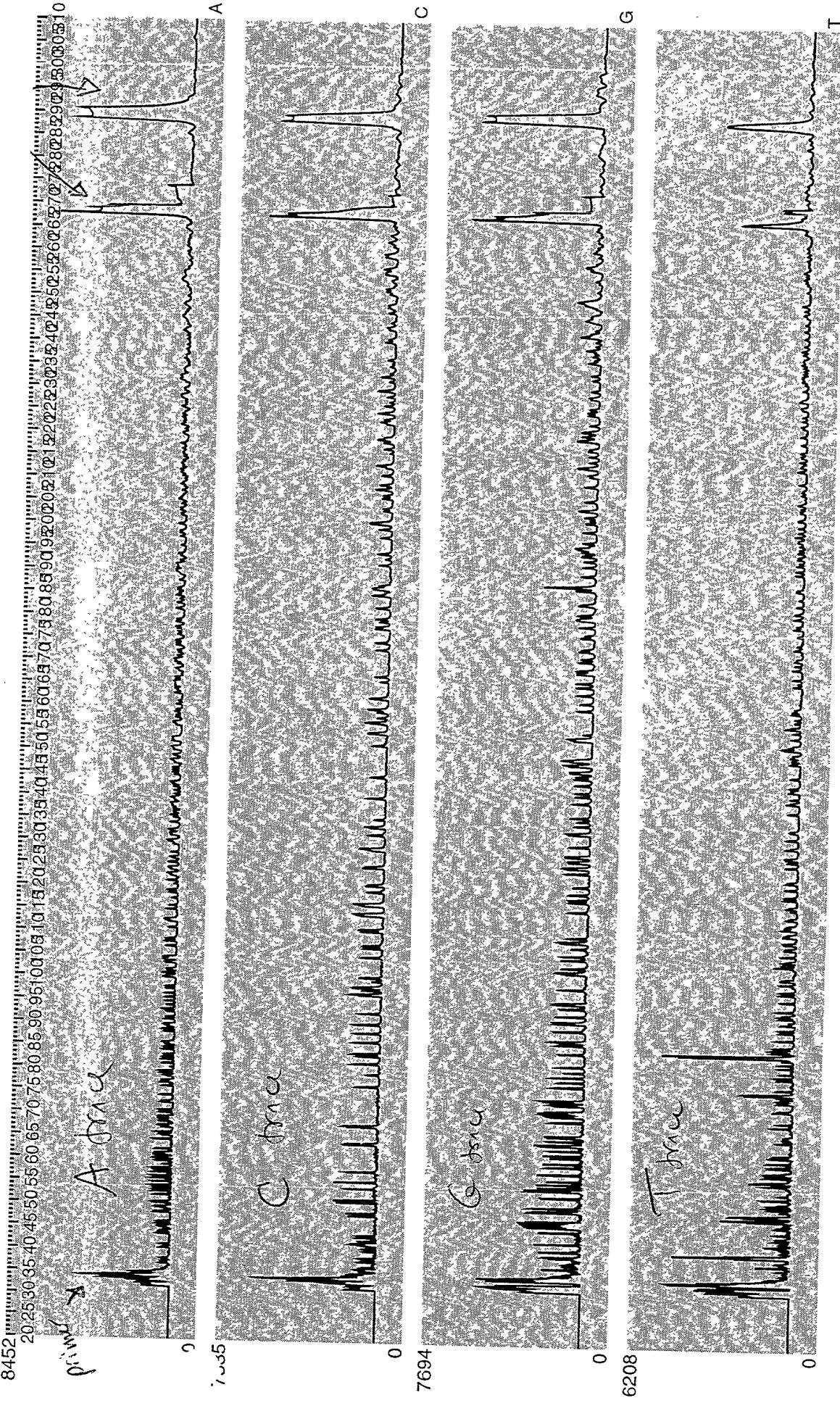


Figure 9A

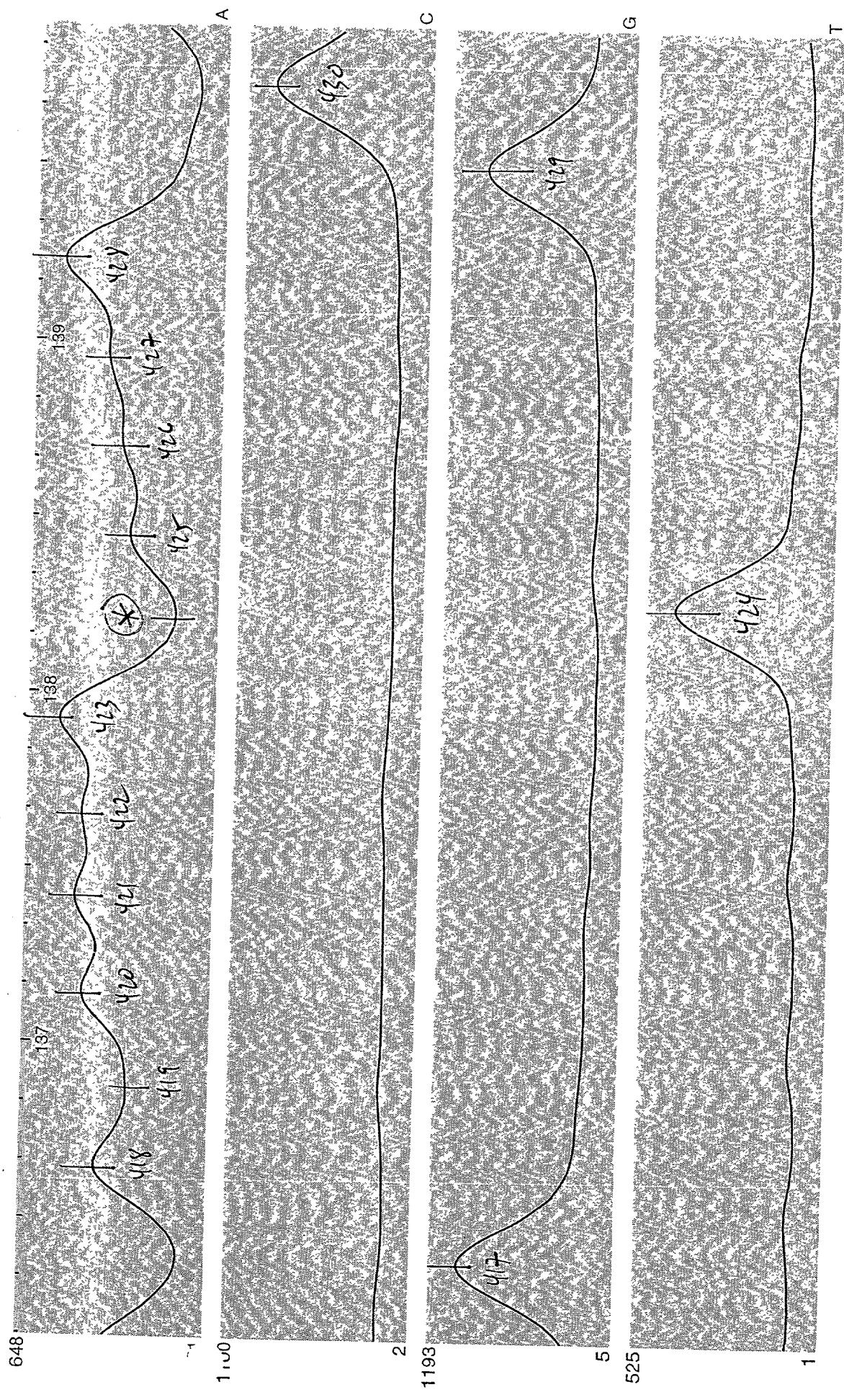


Figure 9B



### Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

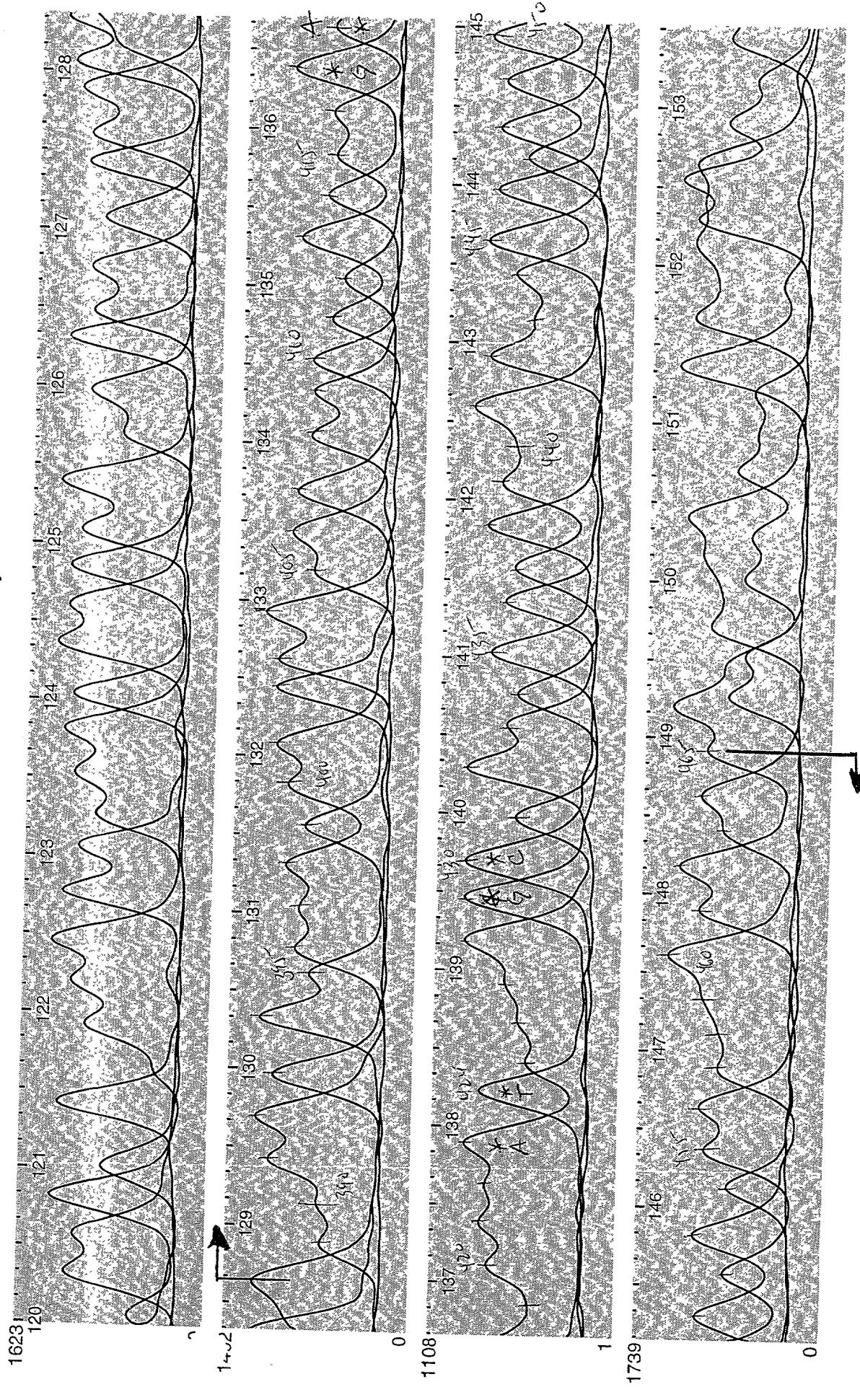


Figure 9

Deviation of the peak position (in number of bases) from the average  
as a function of base number in different traces before alignment

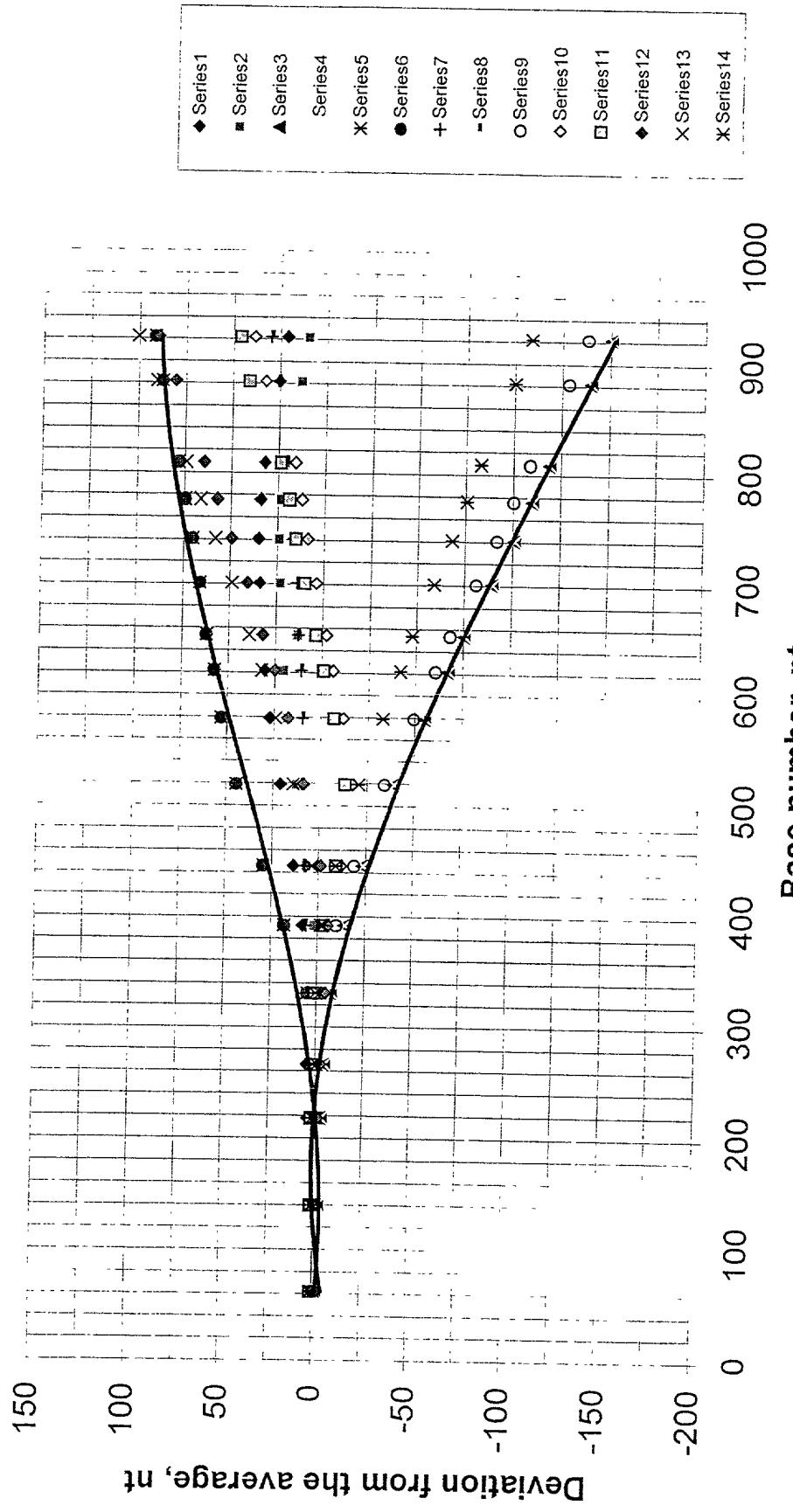


Figure 10

Deviation of the peak position (in number of bases) from the average as a function of base number in the traces aligned with internal standards

(long gel, M13, 5-th degree polynomial) 17 Ref. Peaks

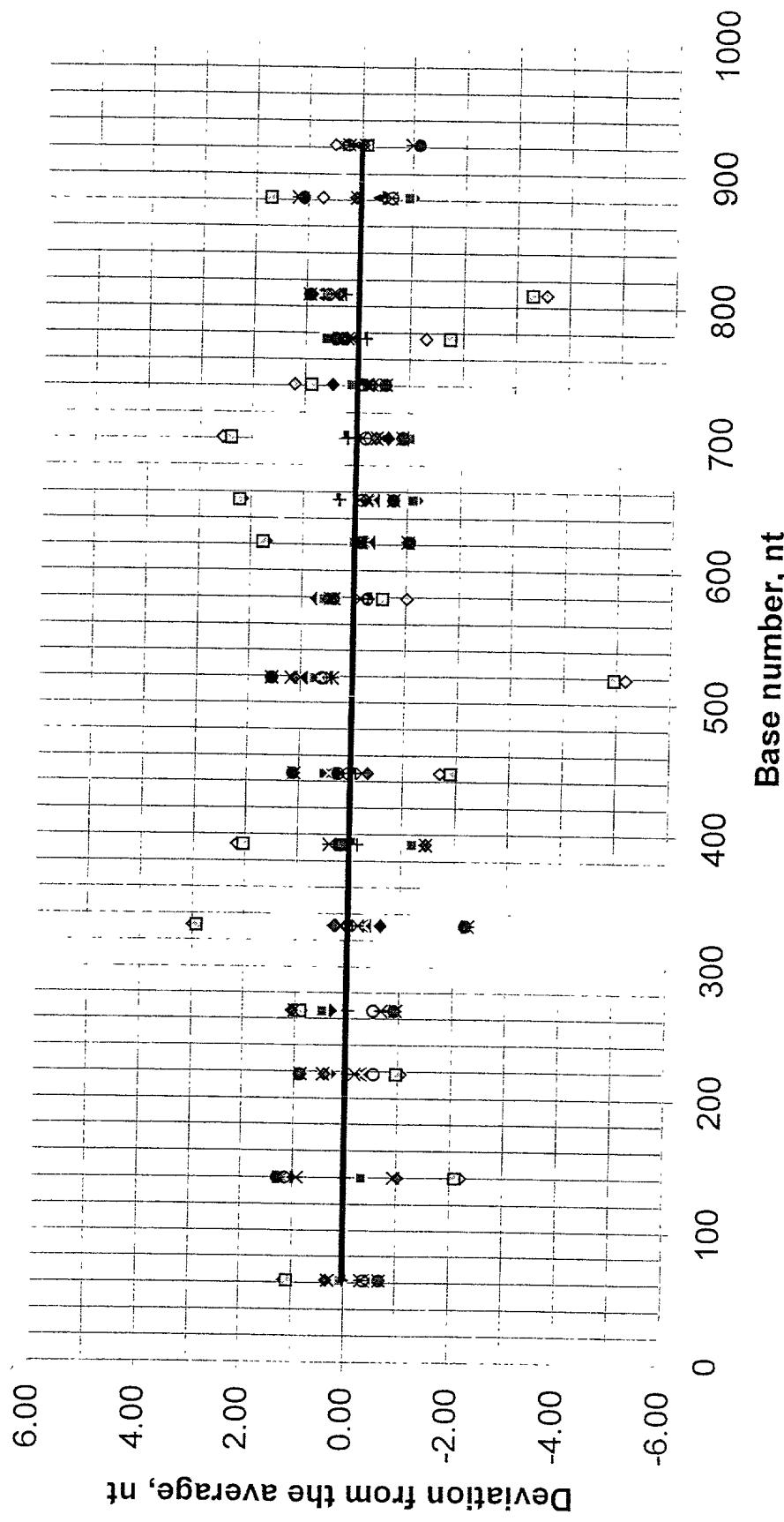


Figure 11

Deviation of the peak position from the average as a function of base number in the traces aligned with internal standards (long gel, M13, 6 peaks, 5-th degree polynomial)

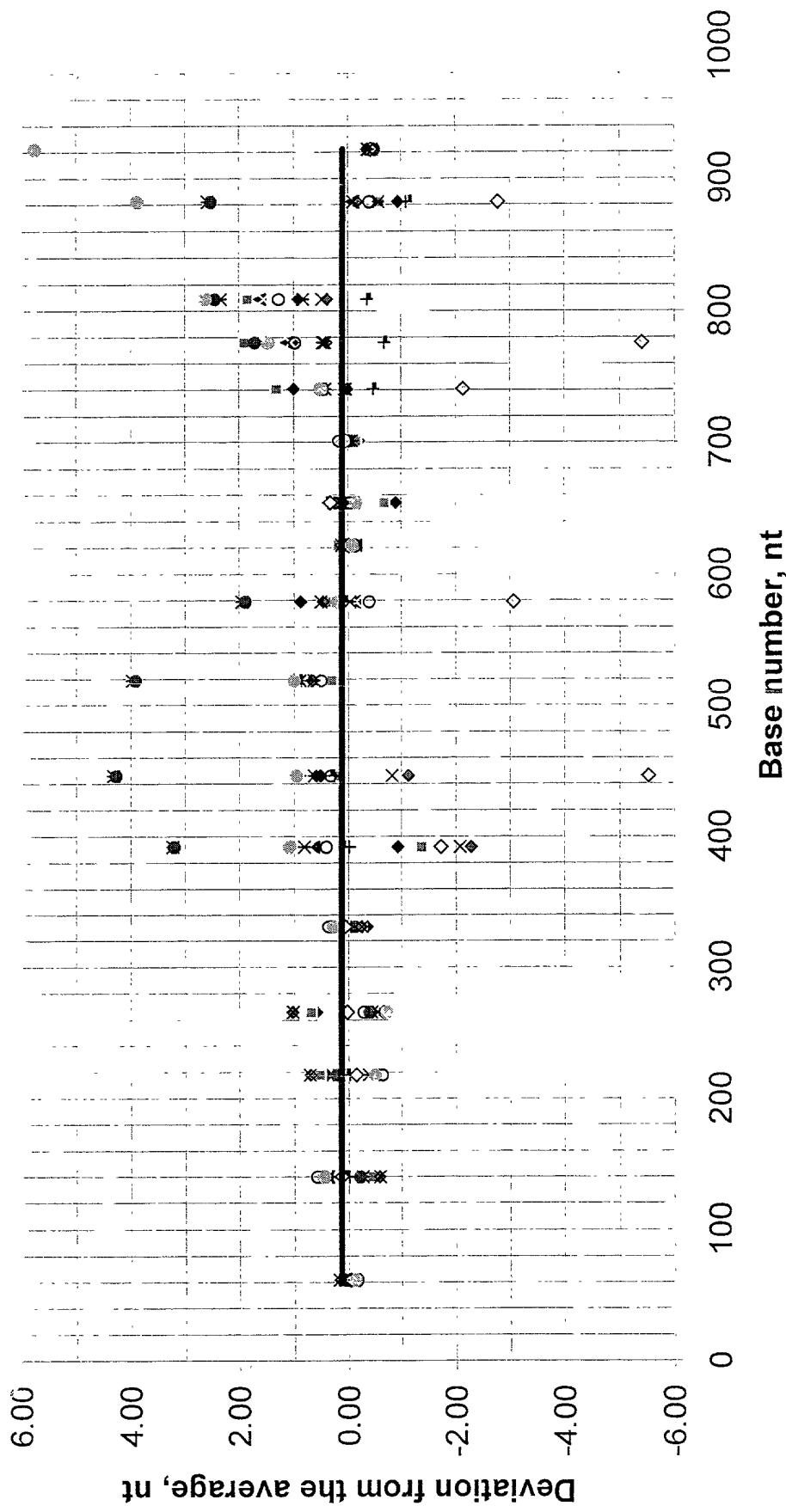


Figure 12